SEQUENCE LISTING

<110> BANYU PHARMACEUTICAL CO., LTD

<120> Method for predicting a drug transport capability by ABCG2 polymorphisms

<130> P2725PCT-GN

<150> JP 2002-175806
<151> 2002-06-17

<160> 68

<170> PatentIn version 3.1

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acc aat ggc ttc ccc gcg aca gct tcc aat gac ctg aag gca ttt act      96
Thr Asn Gly Phe Pro Ala Thr Ala Ser Asn Asp Leu Lys Ala Phe Thr
            20                  25                  30

gaa gga gct gtg tta agt ttt cat aac atc tgc tat cga gta aaa ctg     144
Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
        35                  40                  45

aag agt ggc ttt cta cct tgt cga aaa cca gtt gag aaa gaa ata tta     192
Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
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tcg aat atc aat ggg atc atg aaa cct ggt ctc aac gcc atc ctg gga     240
Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
65                  70                  75                  80

ccc aca ggt gga ggc aaa tct tcg tta tta gat gtc tta gct gca agg     288
Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
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aaa gat cca agt gga tta tct gga gat gtt ctg ata aat gga gca ccg     336
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        115                 120                 125

gtt gtg atg ggc act ctg acg gtg aga gaa aac tta cag ttc tca gca      432
Val Val Met Gly Thr Leu Thr Val Arg Glu Asn Leu Gln Phe Ser Ala
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gct ctt cgg ctt gca aca act atg acg aat cat gaa aaa aac gaa cgg      480
Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
145                 150                 155                 160

att aac agg gtc att caa gag tta ggt ctg gat aaa gtg gca gac tcc      528
Ile Asn Arg Val Ile Gln Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
                165                 170                 175

aag gtt gga act cag ttt atc cgt ggt gtg tct gga gga gaa aga aaa      576
Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
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agg act agt ata gga atg gag ctt atc act gat cct tcc atc ttg ttc      624
Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe
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ttg gat gag cct aca act ggc tta gac tca agc aca gca aat gct gtc      672
Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
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ctt ttg ctc ctg aaa agg atg tct aag cag gga cga aca atc atc ttc      720
Leu Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
225                 230                 235                 240

tcc att cat cag cct cga tat tcc atc ttc aag ttg ttt gat agc ctc      768
Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
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acc tta ttg gcc tca gga aga ctt atg ttc cac ggg cct gct cag gag      816
Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
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gcc ttg gga tac ttt gaa tca gct ggt tat cac tgt gag gcc tat aat      864
Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
        275                 280                 285

aac cct gca gac ttc ttc ttg gac atc att aat gga gat tcc act gct      912
Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
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gtc aac tcc tcc ttc tac aaa gag aca aaa gct gaa tta cat caa ctt     1056
Val Asn Ser Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu
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tcc ggg ggt gag aag aag aag aag atc aca gtc ttc aag gag atc agc     1104
Ser Gly Gly Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser
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tac acc acc tcc ttc tgt cat caa ctc aga tgg gtt tcc aag cgt tca     1152
Tyr Thr Thr Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser
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ttc aaa aac ttg ctg ggt aat ccc cag gcc tct ata gct cag atc att     1200
Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile
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gtc aca gtc gta ctg gga ctg gtt ata ggt gcc att tac ttt ggg cta     1248
Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu
                405                 410                 415

aaa aat gat tct act gga atc cag aac aga gct ggg gtt ctc ttc ttc     1296
Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe
            420                 425                 430

ctg acg acc aac cag tgt ttc agc agt gtt tca gcc gtg gaa ctc ttt     1344
Leu Thr Thr Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe
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gtg gta gag aag aag ctc ttc ata cat gaa tac atc agc gga tac tac     1392
Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr
    450                 455                 460

aga gtg tca tct tat ttc ctt gga aaa ctg tta tct gat tta tta ccc     1440
Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro
465                 470                 475                 480

atg agg atg tta cca agt att ata ttt acc tgt ata gtg tac ttc atg     1488
Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met
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tta gga ttg aag cca aag gca gat gcc ttc ttc gtt atg atg ttt acc     1536
Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr
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gca ggt cag agt gtg gtt tct gta gca aca ctt ctc atg acc atc tgt    1632
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att gca tct tgg ctg tca tgg ctt cag tac ttc agc att cca cga tat    1728
Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr
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gga ttt acg gct ttg cag cat aat gaa ttt ttg gga caa aac ttc tgc    1776
Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys
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cca gga ctc aat gca aca gga aac aat cct tgt aac tat gca aca tgt    1824
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act ggc gaa gaa tat ttg gta aag cag ggc atc gat ctc tca ccc tgg    1872
Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp
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ggc ttg tgg aag aat cac gtg gcc ttg gct tgt atg att gtt att ttc    1920
Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe
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ctc aca att gcc tac ctg aaa ttg tta ttt ctt aaa aaa tat tct taa    1968
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Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
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Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Asp Asp
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Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
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Ile Asn Arg Val Ile Gln Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
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Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
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Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe
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Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
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Leu Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
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Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
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Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
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Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
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Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
290 295 300

Val Ala Leu Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu
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Pro Ser Lys Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr
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